Ecology and surveillance of Listeria monocytogenes on dairy cattle farms

Castro, H.K.

2016

Castro , H K & Lindström , M 2016 , ' Ecology and surveillance of Listeria monocytogenes on dairy cattle farms ' , International Journal of Infectious Diseases , vol. 53 , pp. 68 . https://doi.org/10.1016/j.ijid.2016.1

http://hdl.handle.net/10138/232373
https://doi.org/10.1016/j.ijid.2016.11.171

Conclusion: Presence of G9 and G3 rotavirus genotypes in both water and human samples indicate the possible transmission of rotavirus from contaminated drinking water to humans. This finding corroborates the hypothesis that individuals act as potential reservoir for the spread of rotavirus in the environment. Such information is important for modeling transmission scenarios, identifying risk of food-borne and water-borne virus contamination, and targeting prevention and control efforts in reducing the spread of infection.

http://dx.doi.org/10.1016/j.ijid.2016.11.170

19.109

Ecology and surveillance of *Listeria monocytogenes* on dairy cattle farms

H.K. Castro*, M. Lindström

University of Helsinki, Department of Food Hygiene and Environmental Health, Helsinki/FI

Purpose: Dairy cattle farms serve as reservoirs for *Listeria monocytogenes* and dairy products are a common vehicle for human listeriosis. Understanding *L. monocytogenes* transmission in the dairy farm environment is a prerequisite for the development of control strategies against bulk tank milk contamination. Our aims were to investigate the ecology of *L. monocytogenes* on dairy farms and to examine the utility of in-line milk filter sampling as an economic alternative to bulk tank milk sampling for *L. monocytogenes* screening.

Methods & Materials: We investigated the ecology of *L. monocytogenes* on three Finnish dairy cattle farms in a longitudinal study from late 2013 to early 2016. During this period, we collected a total of 1746 samples from the farm environments, 240 milk filter samples and 207 bulk tank milk samples. *L. monocytogenes* were isolated using a standard two-step enrichment method and identified by PCR. Isolates were genotyped using pulsed-field gel electrophoresis (PFGE) with the restriction enzymes ApaI and AscI and serogrouped using multiplex PCR.

Results: *L. monocytogenes* occurred in the bulk tank milk throughout the year in levels that were consistently small; ≤ 1 – 11 CFU/ml. *L. monocytogenes* was twice more prevalent in milk filters than composite bulk tank milk samples, but the prevalence in milk filters varied notably between farms. Milk filters were poor indicators of bulk tank milk *L. monocytogenes* contamination, with 50% sensitivity and 60% specificity. *L. monocytogenes* presented in the feces of healthy cattle throughout the year, with the prevalence peaking in late spring. In the barn environment, *L. monocytogenes* presented most frequently on floor surfaces, water troughs and feed tables. Each farm environment housed 2 – 3 predominant *L. monocytogenes* genotypes, which were wide-spread and isolated repeatedly for up to 24 months. All predominant genotypes belonged to serogroup 1/2a.

Conclusion: Our findings indicate that milk filter sampling cannot reliably replace bulk tank milk sampling for *L. monocytogenes* screening. Furthermore, persistent genotypes are responsible for the majority of *L. monocytogenes* contamination on dairy farms. Circulation of *Listeria* between the bovine gastrointestinal tract and the farm environment could account for the high prevalence of *L. monocytogenes* observed on cattle farms.

http://dx.doi.org/10.1016/j.ijid.2016.11.171

19.112

Genetic diversity of *Campylobacter jejuni* and *Campylobacter coli* isolates from Austria

S. Jelovcan[a,*], S. Lepuschitz[b], M. Blaschitz[b], M. Selinschek[a], A. Ledolter[a], A. Indra[b], W. Ruppitsch[b], T. Pölzler[a], M. Matt[c]

[a] *AGES Institute for Medical Microbiology and Hygiene / Centre for Foodborne Infectious Diseases, National Reference Centre for Campylobacter, Graz/AT*
[b] *Austrian Agency for Health and Food Safety, Vienna/AT*
[c] *AGES Data, Statistics and Risk Assessment, Innsbruck/AT*

Purpose: *Campylobacter* is the main cause of acute bacterial gastroenteritis in humans in the European Union. In Austria 6.259 cases of campylobacteriosis were reported in 2015. The aim of this study was to determine the genetic diversity of *Campylobacter jejuni* and *Campylobacter coli* isolates from Austria and to identify possible associations between multilocus sequence types and hosts (poultry, food and humans).

Methods & Materials: A total of 283 *Campylobacter* isolates (229 *C. jejuni* and 54 *C. coli* ; 145 human samples, 83 broiler meat/offal samples, 54 poultry samples, and one environmental sample) collected in 2014 were characterized by *in silico* multilocus sequence typing extracted from whole genome sequence data using SeqSphere+ (Ridom, Münster, Germany). The MagnaPure Compact Nucleic Acid Isolation Kit I was used for automated genomic DNA isolation (Roche Diagnostics, Vienna, Austria). The NexteraXT Kit was used for library preparation and 2x300 basepair fragments were sequenced on a MiSeq (Illumina Inc., San Diego, CA, USA) to achieve at least a 70 fold average coverage. Raw reads were *de novo* assembled into a draft genome using Velvet version 1.1.04. Contigs were filtered for a minimum coverage of 5 and minimum length of 200 bp.

Results: The *C. jejuni* isolates had 74 different sequence types (STs) assignable to 21 clonal complexes (CCs) with the major CCs ST-21 CC (n=34), ST-354 CC (n=19), and ST-52 CC (n=18). 11 isolates had new STs and 45 STs were not assignable to CCs. The *C. coli* isolates had 30 different STs assignable to ST-828 CC (n=45), ST-1150 CC (n=2), and no complex (n=7; three with new STs, ST-4148, ST-4743, ST-5150, ST-7993). There were 6 new MLST alleles. *Campylobacter* isolates with identical STs could be found in poultry, food, and humans. 52,1% (*C. jejuni*) and 38,9% (*C. coli*) of STs of human origin matched STs from poultry and/or food.

Conclusion: This study highlights the genetic diversity of *Campylobacter* spp. isolates in Austria. The predominant STs and CCs differ between *C. jejuni* and *C. coli* and sequence types being present in different sources could be found. These findings contribute to a better understanding of the population structure of *Campylobacter* in Austria.

http://dx.doi.org/10.1016/j.ijid.2016.11.172